

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 09/581,528 F  
Source: EFW 16  
Date Processed by STIC: 09/27/2005

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 09/27/2005

PATENT APPLICATION: US/09/581,528F

TIME: 15:21:56

Input Set : A:\P19743.txt

Output Set: N:\CRF4\09272005\I581528F.raw

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3 <110> APPLICANT: TAKEDA, Masatoshi
4     TAKEDA, Junji
6 <120> TITLE OF INVENTION: Gene-Mutated Animal
8 <130> FILE REFERENCE: P19743
10 <140> CURRENT APPLICATION NUMBER: 09/581,528F
11 <141> CURRENT FILING DATE: 2000-10-26
13 <150> PRIOR APPLICATION NUMBER: PCT/JP99/00015
14 <151> PRIOR FILING DATE: 1999-01-07
16 <150> PRIOR APPLICATION NUMBER: JP H10/2191
17 <151> PRIOR FILING DATE: 1998-01-08
19 <160> NUMBER OF SEQ ID NOS: 22
21 <170> SOFTWARE: PatentIn version 3.3
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 467
25 <212> TYPE: PRT
26 <213> ORGANISM: Human
28 <400> SEQUENCE: 1
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31 1          5          10          15
34 Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn Asp Asn
35          20          25          30
38 Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His Pro Glu
39          35          40          45
42 Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val Val Glu
43          50          55          60
46 Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys
47 65          70          75          80
50 His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val
51          85          90          95
54 Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln
55          100         105         110
58 Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg
59          115         120         125
62 Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val
63          130         135         140
66 Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys
67 145         150         155         160
70 Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu Phe Phe
71          165         170         175
74 Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala
75          180         185         190
78 Val Asp Tyr Ile Thr Val Ala Leu Ile Trp Asn Phe Gly Val Val
79          195         200         205

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82 Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala  
 83 210 215 220  
 86 Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr  
 87 225 230 235 240  
 90 Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr  
 91 245 250 255  
 94 Asp Leu Asp Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met Leu Val  
 95 260 265 270  
 98 Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr  
 99 275 280 285  
 102 Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu  
 103 290 295 300  
 106 Ala Gln Arg Arg Val Ser Lys Asn Ser Lys Tyr Asn Ala Glu Ser Thr  
 107 305 310 315 320  
 110 Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe  
 111 325 330 335  
 114 Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg  
 115 340 345 350  
 118 Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile  
 119 355 360 365  
 122 Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly  
 123 370 375 380  
 126 Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala  
 127 385 390 395 400  
 130 Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile  
 131 405 410 415  
 134 Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu  
 135 420 425 430  
 138 Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala  
 139 435 440 445  
 142 Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln  
 143 450 455 460  
 146 Phe Tyr Ile  
 147 465

150 &lt;210&gt; SEQ ID NO: 2

151 &lt;211&gt; LENGTH: 1404

152 &lt;212&gt; TYPE: DNA

153 &lt;213&gt; ORGANISM: Human

155 &lt;400&gt; SEQUENCE: 2

156 atgacagagt tacctgcacc gttgtcctac ttccagaatg cacagatgtc tgaggacaac 60  
 158 cacctgagca atactgtacg tagccagaat gacaatagag aacggcagga gcacaacgac 120  
 160 agacggagcc ttggccaccc tgagccatta tctaattggac gaccccaggg taactcccgg 180  
 162 caggtggtgg agcaagatga ggaagaagat gaggagctga cattgaaata tggcgccaag 240  
 164 catgtgatca tgctctttgt ccctgtgact ctctgcatgg tgggtggtcgt ggctactatt 300  
 166 aagtcagtca gcttttatac ccggaaggat gggcagctaa tctatacccc attcacagaa 360  
 168 gataccgaga ctgtgggcca gagagccctg cactcaattc tgaatgctgc catcatgac 420  
 170 agtgtcattg ttgtcatgac tatectctctg gtggttctgt ataaatacag gtgctataag 480  
 172 gtcacccatg cctggccttat tataatcatct ctattgttgc tgttcttttt ttcattcatt 540  
 174 tacttggggg aagtgtttaa aacctataac gttgctgtgg actacattac tgttgcactc 600

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176 ctgatctgga attttggtgt ggtgggaatg atttccattc actggaaagg tccacttcga      660
178 ctccagcagg catatctcat tatgattagt gccctcatgg ccctgggtgtt tatcaagtac      720
180 ctccctgaat ggaactgcgtg gctcatcttg gctgtgattt cagtatatga tttagtggct      780
182 gttttgtgtc cgaaagggtcc acttcgtatg ctggttgaaa cagctcagga gagaaatgaa      840
184 acgctttttc cagctctcat ttactcctca acaatggtgt ggttggtgaa tatggcagaa      900
186 ggagaccgag aagctcaaag gagagtatcc aaaaattcca agtataatgc agaaagcaca      960
188 gaaagggagt cacaagacac tgttgcagag aatgatgatg gcgggttcag tgaggaatgg     1020
190 gaagcccaga gggacagtca tctagggcct catcgctcta cacctgagtc acgagctgct     1080
192 gtccaggaac tttccagcag taccctcgct ggtgaagacc cagaggaaaag gggagtaaaa     1140
194 cttggattgg gagatttcat tttctacagt gttctggttg gtaaagcctc agcaacagcc     1200
196 agtggagact ggaacacaac catagcctgt ttctagacca tattaattgg tttgtgcctt     1260
198 acattattac tccttgccat tttcaagaaa gcattgccag ctcttccaat ctccatcacc     1320
200 tttgggcttg ttttctactt tgccacagat tatcttgtag agccttttat ggaccaatta     1380
202 gcattccatc aattttatat cttag                                     1404

205 <210> SEQ ID NO: 3
206 <211> LENGTH: 467
207 <212> TYPE: PRT
208 <213> ORGANISM: Mouse
210 <400> SEQUENCE: 3
212 Met Thr Glu Ile Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala Gln Met
213 1          5          10          15
216 Ser Glu Asp Ser His Ser Ser Ser Ala Ile Arg Ser Gln Asn Asp Ser
217          20          25          30
220 Glu Glu Arg Gln Gln Gln His Asp Arg Gln Arg Leu Asp Asn Pro Glu
221          35          40          45
224 Pro Ile Ser Asn Gly Arg Pro Gln Ser Asn Ser Arg Gln Val Val Glu
225          50          55          60
228 Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys
229 65          70          75          80
232 His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val
233          85          90          95
236 Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln
237          100         105         110
240 Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg
241          115         120         125
244 Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val
245          130         135         140
248 Ile Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys
249 145          150         155         160
252 Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu Phe Phe
253          165         170         175
256 Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala
257          180         185         190
260 Val Asp Tyr Val Thr Val Ala Leu Leu Ile Trp Asn Phe Gly Val Val
261          195         200         205
264 Gly Met Ile Ala Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala
265          210         215         220
268 Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr
269 225          230         235         240

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272 Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr  
 273                   245                   250                   255  
 276 Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met Leu Val  
 277                   260                   265                   270  
 280 Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr  
 281                   275                   280                   285  
 284 Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu  
 285           290                   295                   300  
 288 Ala Glu Arg Arg Val Pro Lys Asn Pro Lys Tyr Asn Thr Gln Arg Ala  
 289 305                   310                   315                   320  
 292 Glu Arg Glu Thr Gln Asp Ser Gly Ser Gly Asn Asp Asp Gly Gly Phe  
 293                   325                   330                   335  
 296 Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg  
 297           340                   345                   350  
 300 Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Gly Ser Ile  
 301           355                   360                   365  
 304 Leu Thr Ser Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly  
 305           370                   375                   380  
 308 Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala  
 309 385                   390                   395                   400  
 312 Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile  
 313                   405                   410                   415  
 316 Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu  
 317                   420                   425                   430  
 320 Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala  
 321           435                   440                   445  
 324 Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln  
 325           450                   455                   460  
 328 Phe Tyr Ile  
 329 465

332 &lt;210&gt; SEQ ID NO: 4

333 &lt;211&gt; LENGTH: 1404

334 &lt;212&gt; TYPE: DNA

335 &lt;213&gt; ORGANISM: Mouse

337 &lt;400&gt; SEQUENCE: 4

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338 atgacagaga tacctgcacc tttgtcctac ttccagaatg cccagatgtc tgaggacagc      60
340 cactccagca gcgccatccg gagccagaat gacagccaag aacggcagca gcagcatgac      120
342 aggcagagac ttgacaaccc tgagccaata tctaattgggc ggccccagag taactcaaga      180
344 caggtggtgg aacaagatga ggaggaagac gaagagctga cattgaaata tggagccaag      240
346 catgtcatca tgctctttgt ccccgtagacc ctctgcatgg tcgtcgctcg ggccaccatc      300
348 aaatcagtca gcttctatac ccggaaggac ggtagctaa tctacacccc attcacagaa      360
350 gacactgaga ctgtaggcca aagagccctg cactcgatcc tgaatgcggc catcatgatc      420
352 agtgtcattg tcattatgac catcctcctg gtggtcctgt ataaatacag gtgctacaag      480
354 gtcacccacg cctggcttat tatttcattc ctgttggtgc tgttcttttt ttcgttcatt      540
356 tacttagggg aagtatttaa gacctacaat gtcgccgtgg actacgttac agtagcactc      600
358 ctaatctgga attttggtgt ggtcgggatg attgccatcc actggaaagg ccccttcga      660
360 ctgcagcagg cgtatctcat tatgatcagt gccctcatgg ccttggtatt tatcaagtac      720
362 ctccccgaat ggaccgcatg gctcatcttg gctgtgattt cagtatatga tttggtggct      780
364 gttttatgtc ccaaaggccc acttcgtatg ctggttgaaa cagctcagga aagaaatgag      840

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366 actctctttc cagctcttat ctattcctca acaatgggtg ggttggtgaa tatggctgaa      900
368 ggagacccag aagcccaaag gagggtagcc aagaacccca agtataacac acaaagagcg      960
370 gagagagaga cacaggacag tggttctggg aacgatgatg gtggcttcag tgaggagtgg     1020
372 gagggccaaa gagacagtca cctggggcct catcgctcca ctcccgagtc aagagctgct     1080
374 gtccaggaac tttctgggag cattctaacg agtgaagacc cggaggaaaag aggagtaaaa     1140
376 cttggactgg gagatttcat tttctacagt gttctggttg gtaaggcctc agcaaccgcc     1200
378 agtggagact ggaacacaa catagcctgc tttgtagcca tactgatcgg cctgtgcctt     1260
380 acattactcc tgctcgccat tttcaagaaa gcgttgccag ccctcccatc ctccatcacc     1320
382 ttcgggctcg tgttctactt cgccacggat taccttgtgc agcccttcat ggaccaactt     1380
384 gcattccatc agttttatat ctag                                     1404
387 <210> SEQ ID NO: 5
388 <211> LENGTH: 25
389 <212> TYPE: DNA
390 <213> ORGANISM: Artificial
392 <220> FEATURE:
393 <223> OTHER INFORMATION: Primer
395 <400> SEQUENCE: 5
396 ggaattttgg tgtggtcggg atgat                                     25
399 <210> SEQ ID NO: 6
400 <211> LENGTH: 23
401 <212> TYPE: DNA
402 <213> ORGANISM: Artificial
404 <220> FEATURE:
405 <223> OTHER INFORMATION: Primer
407 <400> SEQUENCE: 6
408 ggtccattcg gggaggtact tga                                     23
411 <210> SEQ ID NO: 7
412 <211> LENGTH: 36
413 <212> TYPE: DNA
414 <213> ORGANISM: Artificial
416 <220> FEATURE:
417 <223> OTHER INFORMATION: Primer
419 <400> SEQUENCE: 7
420 tgtggtcggg atgatcgcca cccactggaa aggccc                                     36
423 <210> SEQ ID NO: 8
424 <211> LENGTH: 36
425 <212> TYPE: DNA
426 <213> ORGANISM: Artificial
428 <220> FEATURE:
429 <223> OTHER INFORMATION: Primer
431 <400> SEQUENCE: 8
432 gggcctttcc agtgggtggc gatcatcccg accaca                                     36
435 <210> SEQ ID NO: 9
436 <211> LENGTH: 18
437 <212> TYPE: DNA
438 <213> ORGANISM: Artificial
440 <220> FEATURE:
441 <223> OTHER INFORMATION: Primer
443 <400> SEQUENCE: 9

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/581,528F

DATE: 09/27/2005  
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Input Set : A:\P19743.txt  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:20; N Pos. 20,21,22

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22

**VERIFICATION SUMMARY**

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L:614 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0